AMENDMENTS TO THE SPECIFICATION:

Please amend this application on page 1, line 1, by inserting the following new paragraph:

This is a division of Application No. 09/742,361, filed December 22, 2003, which is a continuation of International Application No. PCT/EP99/04490, filed June 29, 1999, which in turn is a continuation-in-part of U.S. application No. 09/107,383, filed June 30, 1988, now U.S. Patent No. 6,190,667, all of which are incorporated herein by reference.

Please replace the second paragraph on page 3 with the following paragraph:

Figure 2A depicts a restriction map of pILL823, pILL824, pILL833 and pILL834. Small boxes mark the vector of each plasmid, and large boxes correspond to genes. *Ori* indicates the position of the ColE1 origin of replication. Sp^R *and* Ap^R are the genes conferring resistance to spectinomycin and ampicillin, respectively. Cassettes inserted into *ureI* and conferring resistance to chloramphenicol (*cat*) or kanamycin (*aphA-3*) are also shown. The sequence of the DNA region (SEQ ID NO: 17) comprising the *ureI* stop codon and the *ureE* start codon, including the *BclI* site where adaptor H19 (SEQ ID NO: 18) was inserted, is given. Insertion of H19 into the *Bcl*I site of pILL824 produced pILL825, the resulting *ureI-ureE* intergenic region is also shown. The stop codon of *ureI* and the start codon of *ureE* are boxed and the ribosome binding site (RBS) is underlined. Brackets indicate the position of restriction sites removed by ligation.

Please replace the first paragraph on page 4 with the following paragraph:

Figure 3 shows the alignment of the amino acid sequence of UreI from *H. pylori* with those of similar proteins and prediction of the two-dimensional structure of members of the UreI/AmiS protein family. Residues identical at one position in, at least,

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four sequences are boxed and dashes indicate gaps inserted to optimize alignment. The organisms from which the sequences originated and the degree of identity with the *H. pylori* UreI protein are: UreI-Hp, *Helicocobacter pylori* (195 residues, accession No. M84338) (SEQ ID NO: 10); UreI-Hf, *Helicobacter felis* (74% identity over 196 residues, accession No. A41012) (SEQ ID NO: 11); UreI-Lacto, *Lactobacillus fermentum* (55% identity over the 46 residues-long partial sequence, accession No. D10605) (SEQ ID NO: 12); UreI-Strepto, *Streptococcus salivarius* (54% identity over the 129 residues-long partial sequence, accession No. U35248) (SEQ ID NO: 13); AmiS-Myco, *Mycobacterium smegmatis* (39% identity over 172 residues, accession No. X57175) (SEQ ID NO: 14); AmiS-Rhod, *Rhodococcus* sp. R312 (37% identity over 172 residues, accession No. Z46523) (SEQ ID NO: 15), and AmiS-Pseudo, *Pseudomonas aeruginosa* (37% identity over 171 residues, accession No. X77161) (SEQ ID NO: 16). Predicted transmembrane -helices are shown as shaded boxes. The regions separating these boxes are hydrophilic loops labeled "IN" when predicted to be intracellular and "OUT" when predicted to be extracellular.

Please enter the substitute Sequence Listing submitted concurrently with this Amendment into the specification.

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